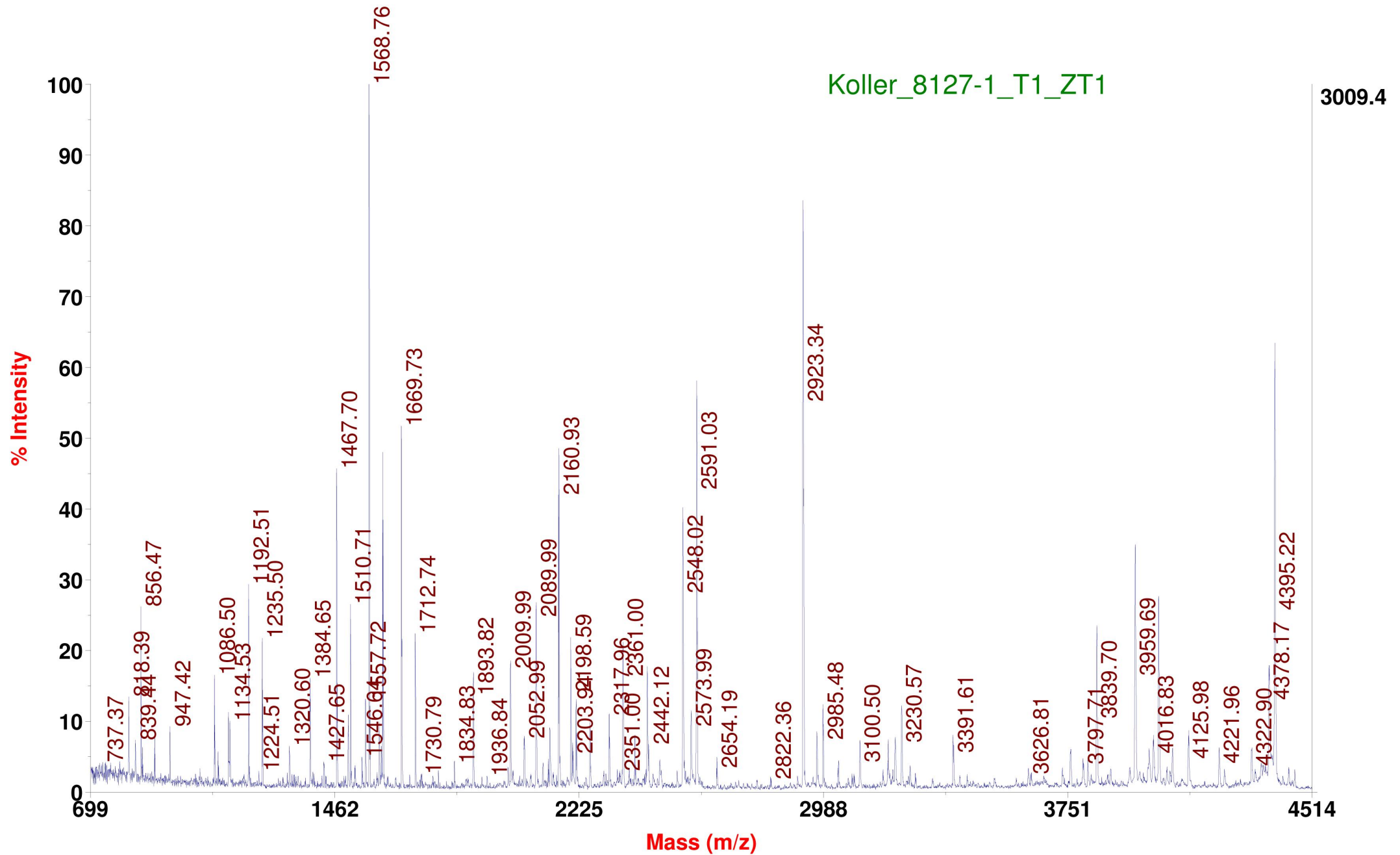


4700 Reflector Spec #1 MC[BP = 1568.8, 3009]





Mascot Search Results

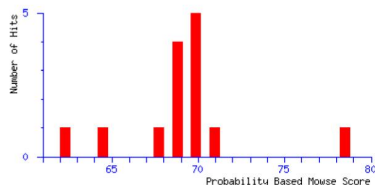
red arrow - N - terminal peptide

blue arrow - C - terminal peptide

User :
 Email :
 Search title : P9_MS_1.t2d - Koller_8127-1_T1_ZT1
 Database : Steffi 1 (14 sequences; 4130 residues)
 Timestamp : 1 Dec 2016 at 07:48:00 GMT
 Top Score : 79 for **Protease_1_94-372**,

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 24 are significant ($p < 0.05$).





Protein Summary Report

Format As [Help](#)
 Significance threshold $p <$ Max. number of hits

Index

Accession	Mass	Score	Description
1. Protease 1 94-372	28361	79	
2. Protease 1 94-366	27714	70	
3. Protease 1 94-367	27827	70	
4. Protease 1 94-368	27940	70	
5. Protease 1 94-369	28103	70	
6. Protease 1 94-370	28217	70	
7. Protease 1 94-371	28274	70	
8. Protease 1 94-373	28418	69	
9. Protease 1 94-374	28546	69	
10. Protease 1 94-375	28603	69	
11. Protease 1 94-376	28690	69	
12. Protease 1 94-382	29512	68	
13. Protease 1 full length 1-382	39937	64	
14. Protease 1 full length plus Signal peptide	41853	62	

Results List

1.	Protease 1 94-372	Mass: 28361	Score: 79	Expect: 2e-007	Queries matched: 12			
	Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
	856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
	947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.L
	1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
	1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
	1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
	1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGLGR.I 
	1594.6986	1593.6913	1593.7747	-0.0833	265	- 279	1	R.NPGTSTTNRLLYNGS.-
	1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.L
	2089.9856	2088.9783	2089.0551	-0.0768	131	- 151	0	K.AALNLSLGGFNPQATNDVTR.A
	2923.3357	2922.3284	2922.4147	-0.0863	194	- 222	0	K.SSFSNWGSIVDIYAPGSNIISDAPGGVVR.T
	3203.3560	3202.3487	3202.4449	-0.0962	223	- 254	0	R.TMSGTSMASPHVCAGAAMLAQGVVPGQVCDR.L
	3811.7322	3810.7249	3810.7760	-0.0511	20	- 55	1	R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
	No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							
2.	Protease 1 94-366	Mass: 27714	Score: 70	Expect: 1.3e-006	Queries matched: 11			
	Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
	856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
	947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.-
	1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
	1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
	1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
	1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGLGR.I 
	1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.-

2089.9856 2088.9783 2089.0551 -0.0768 131 - 151 0 K.AALNLSLGGGFNQATNDVAVTR.A
 2923.3357 2922.3284 2922.4147 -0.0863 194 - 222 0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGV.R
 3203.3560 3202.3487 3202.4449 -0.0962 223 - 254 0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
 3811.7322 3810.7249 3810.7760 -0.0511 20 - 55 1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGG.R
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231

3. [Protease 1 94-367](#) Mass: 27827 Score: 70 Expect: 1.3e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVTDR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGV.R
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGG.R

No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231

4. [Protease 1 94-368](#) Mass: 27940 Score: 70 Expect: 1.4e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVTDR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGV.R
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGG.R

No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231

5. [Protease 1 94-369](#) Mass: 28103 Score: 70 Expect: 1.4e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVTDR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGV.R
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGG.R

No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231

3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819,
3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639,
4322.8979, 4377.2358, 4378.1675, 4395.2231

6. [Protease 1 94-370](#) Mass: 28217 Score: 70 Expect: 1.5e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	- 151	0	K.AALNLSLGGGFNQATNDVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	- 222	0	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	- 254	0	R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	- 55	1	R.SPGNKDFVYDDTAGQGITYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

7. [Protease 1 94-371](#) Mass: 28274 Score: 70 Expect: 1.5e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	- 151	0	K.AALNLSLGGGFNQATNDVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	- 222	0	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	- 254	0	R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	- 55	1	R.SPGNKDFVYDDTAGQGITYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

8. [Protease 1 94-373](#) Mass: 28418 Score: 69 Expect: 1.6e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	- 151	0	K.AALNLSLGGGFNQATNDVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	- 222	0	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	- 254	0	R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	- 55	1	R.SPGNKDFVYDDTAGQGITYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

9. [Protease 1 94-374](#) Mass: 28546 Score: 69 Expect: 1.7e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	- 264	0	K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	- 273	0	R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	- 264	1	R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	- 123	0	K.GIDWCVTDAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	- 113	0	K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	- 15	0	-.ALTTQPNAPSWGGLGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	- 273	1	K.QIGNAVVRNPGTSTTNR.L

2089.9856 2088.9783 2089.0551 -0.0768 131 - 151 0 K.AALNLSLGGGFNQATNDVAVTR.A
 2923.3357 2922.3284 2922.4147 -0.0863 194 - 222 0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
 3203.3560 3202.3487 3202.4449 -0.0962 223 - 254 0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
 3811.7322 3810.7249 3810.7760 -0.0511 20 - 55 1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231

10. [Protease 1 94-375](#) Mass: 28603 Score: 69 Expect: 1.8e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVT DAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWG LGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

11. [Protease 1 94-376](#) Mass: 28690 Score: 69 Expect: 1.8e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVT DAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWG LGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

12. [Protease 1 94-382](#) Mass: 29512 Score: 68 Expect: 2.2e-006 Queries matched: 11

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
856.4697	855.4624	855.4926	-0.0302	257	-	264	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	265	-	273	0 R.NPGTSTTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	255	-	264	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	114	-	123	0 K.GIDWCVT DAR.S
1346.6834	1345.6761	1345.7201	-0.0440	99	-	113	0 K.VLSASGSGSNAGVIK.G
1568.7599	1567.7526	1567.8107	-0.0580	1	-	15	0 -.ALTTQPNAPSWG LGR.I ←
1784.8785	1783.8713	1783.9288	-0.0576	257	-	273	1 K.QIGNAVVRNPGTSTTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	131	-	151	0 K.AALNLSLGGGFNQATNDVAVTR.A
2923.3357	2922.3284	2922.4147	-0.0863	194	-	222	0 K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	223	-	254	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	20	-	55	1 R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.3948, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2380.0496, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954,
3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819,
3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639,
4322.8979, 4377.2358, 4378.1675, 4395.2231

13. [Protease 1 full length 1-382](#) Mass: 39937 Score: 64 Expect: 5.2e-006 Queries matched: 12

Observed	Mr (exp't)	Mr (calc)	Delta	Start	End	Miss	Peptide
818.3948	817.3876	817.3718	0.0157	83	-	88	0 K.YVEHDR.V
856.4697	855.4624	855.4926	-0.0302	350	-	357	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	358	-	366	0 R.NPGTSTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	348	-	357	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	207	-	216	0 K.GIDWCVTDA.R.S
1346.6834	1345.6761	1345.7201	-0.0440	192	-	206	0 K.VLSASGSGSNAGVIK.G
1784.8785	1783.8713	1783.9288	-0.0576	350	-	366	1 K.QIGNAVVRNPGTSTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	224	-	244	0 K.AALNLSLGGGFNQATNDVTR.A
2380.0496	2379.0423	2379.2044	-0.1622	2	-	22	1 R.AFFHNKGGNDIIPNSYIVVMK.D + Oxidation (M)
2923.3357	2922.3284	2922.4147	-0.0863	287	-	315	0 K.SSFSNWGSIVDIYAPGNSIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	316	-	347	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPVGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	113	-	148	1 R.SPGNKDFVYDDTAGQGITYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1568.7599, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

14. [Protease 1 full length plus Signal peptide](#) Mass: 41853 Score: 62 Expect: 8.2e-006 Queries matched: 12

Observed	Mr (exp't)	Mr (calc)	Delta	Start	End	Miss	Peptide
818.3948	817.3876	817.3718	0.0157	102	-	107	0 K.YVEHDR.V
856.4697	855.4624	855.4926	-0.0302	369	-	376	0 K.QIGNAVVR.N
947.4228	946.4155	946.4468	-0.0313	377	-	385	0 R.NPGTSTNR.L
1097.6431	1096.6358	1096.6716	-0.0358	367	-	376	1 R.LKQIGNAVVR.N
1192.5066	1191.4993	1191.5342	-0.0349	226	-	235	0 K.GIDWCVTDA.R.S
1346.6834	1345.6761	1345.7201	-0.0440	211	-	225	0 K.VLSASGSGSNAGVIK.G
1784.8785	1783.8713	1783.9288	-0.0576	369	-	385	1 K.QIGNAVVRNPGTSTNR.L
2089.9856	2088.9783	2089.0551	-0.0768	243	-	263	0 K.AALNLSLGGGFNQATNDVTR.A
2380.0496	2379.0423	2379.2044	-0.1622	21	-	41	1 R.AFFHNKGGNDIIPNSYIVVMK.D + Oxidation (M)
2923.3357	2922.3284	2922.4147	-0.0863	306	-	334	0 K.SSFSNWGSIVDIYAPGNSIISDAPGGGVR.T
3203.3560	3202.3487	3202.4449	-0.0962	335	-	366	0 R.TMSGTSMASPHVCGAGAAMLAQGVVPVGVQVCDR.L
3811.7322	3810.7249	3810.7760	-0.0511	132	-	167	1 R.SPGNKDFVYDDTAGQGITYGVDTGIDINHPDFGGR.A
No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 839.4433, 858.4949, 859.4981, 861.3915, 899.4702, 1086.5004, 1129.5076, 1132.5085, 1133.4841, 1134.5315, 1224.5101, 1235.5029, 1313.6464, 1320.5973, 1334.6139, 1384.6472, 1393.6626, 1427.6527, 1433.7258, 1467.7009, 1503.6478, 1510.7076, 1524.6400, 1546.6444, 1557.7217, 1568.7599, 1594.6986, 1600.7336, 1605.7229, 1607.7161, 1611.7679, 1669.7307, 1712.7358, 1730.7920, 1767.8136, 1834.8348, 1893.8197, 1936.8419, 2002.8632, 2009.9857, 2052.9927, 2110.9190, 2127.9177, 2132.9998, 2142.9309, 2160.9346, 2198.0662, 2198.5911, 2203.9448, 2215.0576, 2258.0129, 2317.9634, 2351.0039, 2359.0432, 2360.9961, 2398.1003, 2433.0029, 2436.9856, 2441.0759, 2442.1169, 2476.0034, 2547.0313, 2548.0212, 2553.1460, 2573.9905, 2591.0327, 2654.1919, 2822.3552, 2922.3638, 2966.3379, 2985.4771, 3033.4314, 3076.4116, 3083.3225, 3100.4958, 3173.6069, 3188.4954, 3210.4119, 3230.5667, 3253.4275, 3257.3911, 3274.5586, 3391.6094, 3626.8101, 3634.5938, 3733.6704, 3757.6819, 3797.7144, 3839.6951, 3959.6892, 4000.7944, 4005.7834, 4016.8291, 4032.7107, 4075.7166, 4125.9771, 4221.9639, 4322.8979, 4377.2358, 4378.1675, 4395.2231							

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : Carbamidomethyl (C)
 Variable modifications : Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 100 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 126

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: **Protease_1_94-372** Score: **79** Expect: **2e-007**

Nominal mass (M_r): **28361**; Calculated pI value: **8.70**
 NCBI BLAST search of [Protease_1_94-372](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Number of mass values searched: **126**
 Number of mass values matched: **12**
 Sequence Coverage: **65%**

Matched peptides shown in **Bold Red**

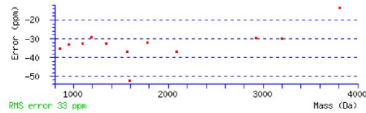
1 ALTTQPNAPS WGLGRISHRS **PGNKDFVYDD TAGQGITIYG VDTGIDINHP**
51 DFGGRARWGT NTVDNANNDG HGHGTHTAGT FAGNAYGIAR KASVVAVK**VL**
101 SASGSGSNAG VIKGIDWCVT DARSKGALGK **AALNLSLGGG FNQATNDAVT**
151 RAQTAGIFVA VAAAGNDNKDA RNYSPASAPA VCTVASSTID **DQKSSFSNWG**
201 SIVDIYAPGS NIISDAPGGG VRTMSGTSMA SPHVCAGAA MLRQGVFVQ
251 VCDRLKQIGN AVVRNPGTST TNRLLYNGS

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start	End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1	15	1568.7599	1567.7526	1567.8107	-0.0580	0	-.ALTTQPNAPSWGLGR.I ←
20	55	3811.7322	3810.7249	3810.7760	-0.0511	1	R.SPGNKDFVYDDTAGQGITIYGVDTGIDINHPDFGGR.A
99	113	1346.6834	1345.6761	1345.7201	-0.0440	0	K.VLSASGSGSNAGVIK.G
114	123	1192.5066	1191.4993	1191.5342	-0.0349	0	K.GIDWCVTDR.S
131	151	2089.9856	2088.9783	2089.0551	-0.0768	0	K.AALNLSLGGGFNQATNDAVTR.A
194	222	2923.3357	2922.3284	2922.4147	-0.0863	0	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.T
223	254	3203.3560	3202.3487	3202.4449	-0.0962	0	R.TMSGTSMASPHVCAGAAAMLRQGVFVQVCDR.L
255	264	1097.6431	1096.6358	1096.6716	-0.0358	1	R.LKQIGNAVVR.N
257	264	856.4697	855.4624	855.4926	-0.0302	0	K.QIGNAVVR.N
257	273	1784.8785	1783.8713	1783.9288	-0.0576	1	K.QIGNAVVRNPGTSTTNR.L
265	273	947.4228	946.4155	946.4468	-0.0313	0	R.NPGTSTTNR.L
265	279	1594.6986	1593.6913	1593.7747	-0.0833	1	R.NPGTSTTNRLLYNGS.- ←

No match to: 724.4434, 733.4623, 737.3729, 744.4733, 746.4565, 749.4891, 755.4316, 760.4791, 762.5109, 768.4706, 786.5005, 790.5098, 798.4902, 818.



RMS error: 33 ppm

Mascot: <http://www.matrixscience.com/>

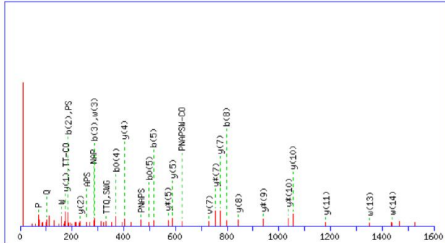
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALTTQPNAPSWGLGR**
 Found in **Protease_1_94-366**

Match to Query 1: 1567.752724 from(1568.760000,1+)

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da



Monoisotopic mass of neutral peptide Mr(calc): 1567.8107

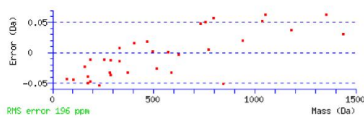
Fixed modifications: Carbamidomethyl (C)

Ions Score: 56 Expect: 1.5e-006

Matches (Bold Red): 35/256 fragment ions using 39 most intense peaks

#	Immon.	a	a*	a ⁰	b	b*	b ⁰	Seq.	v	w	w'	y	y*	y ⁰	#
1	44.0495	44.0495			72.0444			A							15
2	86.0964	157.1335			185.1284			L	1439.7026	1438.7073		1497.7808	1480.7543	1479.7703	14
3	74.0600	258.1812		240.1706	286.1761		268.1656	T	1338.6549	1351.6753	1353.6546	1384.6968	1367.6702	1366.6862	13
4	74.0600	359.2289		341.2183	387.2238		369.2132	T	1237.6072	1250.6276	1252.6069	1283.6491	1266.6225	1265.6385	12
5	101.0709	487.2875	470.2609	469.2769	515.2824	498.2558	497.2718	Q	1109.5486	1108.5534		1182.6014	1165.5749	1164.5908	11
6	70.0651	584.3402	567.3137	566.3297	612.3351	595.3086	594.3246	P	1012.4959	1011.5006		1054.5428	1037.5163	1036.5323	10
7	87.0553	698.3832	681.3566	680.3726	726.3781	709.3515	708.3675	N	898.4530	897.4577		957.4901	940.4635	939.4795	9
8	44.0495	769.4203	752.3937	751.4097	797.4152	780.3886	779.4046	A	827.4158			843.4471	826.4206	825.4366	8
9	70.0651	866.4730	849.4465	848.4625	894.4679	877.4414	876.4574	P	730.3631	729.3678		772.4100	755.3835	754.3995	7
10	60.0444	953.5051	936.4785	935.4945	981.5000	964.4734	963.4894	S	643.3311	642.3358		675.3573	658.3307	657.3467	6
11	159.0917	1139.5844	1122.5578	1121.5738	1167.5793	1150.5527	1149.5687	W	457.2517			588.3252	571.2987		5
12	30.0338	1196.6058	1179.5793	1178.5953	1224.6007	1207.5742	1206.5902	G				402.2459	385.2194		4
13	86.0964	1309.6899	1292.6633	1291.6793	1337.6848	1320.6583	1319.6742	L	287.1462	286.1510		345.2245	328.1979		3
14	30.0338	1366.7114	1349.6848	1348.7008	1394.7063	1377.6797	1376.6957	G				232.1404	215.1139		2
15	129.1135							R	74.0237	73.0284		175.1190	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LT	187.1441	215.1390	LTT	288.1918	316.1867	LTTQ	416.2504	444.2453
LTTQP	513.3031	541.2980	LTTQPN	627.3461	655.3410	LTTQPNA	698.3832	726.3781
TT	175.1077	203.1026	TTQ	303.1663	331.1612	TTQP	400.2191	428.2140
TTQPN	514.2620	542.2569	TTQPNA	585.2991	613.2940	TTQP NAP	682.3519	710.3468
TQ	202.1186	230.1135	TQP	299.1714	327.1663	TQPN	413.2143	441.2092
TQPNA	484.2514	512.2463	TQP NAP	581.3042	609.2991	TQP NAPS	668.3362	696.3311
QP	198.1237	226.1186	QPN	312.1666	340.1615	QPNA	383.2037	411.1987
QPNAP	480.2565	508.2514	QPNAPS	567.2885	595.2834	PN	184.1081	212.1030
PNA	255.1452	283.1401	PNAP	352.1979	380.1928	PNAPS	439.2300	467.2249
PNAPSW	625.3093	653.3042	PNAPSWG	682.3307	710.3256	NA	158.0924	186.0873
NAP	255.1452	283.1401	NAPS	342.1772	370.1721	NAPSW	528.2565	556.2514
NAPSWG	585.2780	613.2729	NAPSWG L	698.3620	726.3569	AP	141.1022	169.0971
APS	228.1343	256.1292	APSW	414.2136	442.2085	APSWG	471.2350	499.2299
APSWG L	584.3191	612.3140	APSWG L G	641.3406	669.3355	PS	157.0972	185.0921
PSW	343.1765	371.1714	PSWG	400.1979	428.1928	PSWGL	513.2820	541.2769
PSWGL G	570.3034	598.2984	SW	246.1237	274.1186	SWG	303.1452	331.1401
SWGL	416.2292	444.2241	SWGL G	473.2507	501.2456	WG	216.1131	244.1080
WGL	329.1972	357.1921	WGL G	386.2187	414.2136	GL	143.1179	171.1128
GLG	200.1393	228.1343	LG	143.1179	171.1128			



NCBI BLAST search of **ALTTQPNAPSWGLGR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

Mascot: <http://www.matrixscience.com/>